

Sup Table 1A. Long-range PCR primers and conditions

Gene region	Nucleotide position	Length (bp)	Intergenic region	Primer name	Primer sequence	Annealing Temp. (oC)	Amplified Length (bp)	Included exon	Number of Sequencing primer
<i>BG1</i>	129025 - 132794	3770		BG1_F4	GCAAAGATTGATGCTGGGTGTAGCC	68	4531	<i>BG1_e1~e16</i>	22 (Fwd: 11, Rev: 11)
				BG1_R46	GATACGTGGTCACACTGTTCCCAAA				
<i>Blec4</i>	133807 - 135856	2050		Blec4_F	CCGGTGCTGGATCCATCTGATGTCTG	68	4450		20 (Fwd: 10, Rev: 10)
				Blec4_R	TGGAGGGCGACGTCTGTAGTGGTGAA				
<i>Blec2</i>	136593 - 139085	2493		Blec2_F2	CAGAACCGCTGCTTTCCTTGACACA	68	4359	<i>Blec2_e1~e6</i>	19 (Fwd: 10, Rev: 9)
				Blec2_R3	GTCCGCTGATGCTGAATGCGAAAAT				
<i>Blec1</i>	140952 - 143025	2074		Blec1_F3	CATCATCTGCTTCATTTCCAATCCCC	68	3598	<i>Blec1_e1~e5</i>	21 (Fwd: 11, Rev: 10)
				Blec1_R1	TTCCTGTGACAAAACACCGTTAAAAGTGA				
<i>BLB1</i>	143849 - 145212	1364		BLB1_SF2	GGCGGAGCTTCGGCTCCAAATTACAT	68	2421	<i>BLB1_e1~e6</i>	22 (Fwd: 13, Rev: 9)
				BLB1_SR2	CATGAGGGGATCATGAAGGGGCAGAG				
			<i>BLB1-TAPBP</i>	BLB1_SF3	TCACCCGTCTCCAGGCAGAGTT	68	1353		8 (Fwd: 5, Rev: 3)
				BLB1_SR3	GACAATGGGAGATCATGGATTGGGT				
<i>TAPBP</i>	146197 - 149646	3450		Tapasin_F1	TCTACCTGGACTTGTGTGCGGCCATT	68	4191	<i>TAPBP_e1~e8</i>	35 (Fwd: 18, Rev: 17)
				Tapasin_R2	ACTCATCTGCCTCACCAACCCAGGA				
<i>BLB2</i>	150683 - 152034	1352		BLB2_F2s	CTCTCCGCTGCTTTGCGCTTT	68	2484	<i>BLB2_e1~e6</i>	19 (Fwd: 9, Rev: 10)
				BLB2_R3s	GCGACATCTCCAACGGACG				
			<i>BLB2-BRD2</i>	BLB2_SF1_2	TGACCTCGTCTCGCTGTGTTTCAGG	68	1524		6 (Fwd: 4, Rev: 10)
				BLB2_SR1	GACTCGGATTCGGGTAAACCCAC				
<i>BRD2</i>	153386 - 157147			BRD2_F2	GGCCGGGCGAGCTCCAATAAATAAAAC	68	4286	<i>BRD2_e1~e11</i>	15 (Fwd: 8, Rev: 7)
				BRD2_R2	CGACGGAATCGACCCCGGG				
			<i>BRD2-DMA-1</i>	BRD2-DMA-1_F1	CTCTGGGCTTTAAATCCTTGGGCGC	68	3720		12 (Fwd: 6, Rev: 6)
				BRD2-DMA-1_R1	ATTACCTCAGGACCCCTTCCAGGATCCCC				
			<i>BRD2-DMA-2</i>	BRD2-DMA-2_F1	ATCCCCGGTTCATAACTGCCAACACC	68	3684		11 (Fwd: 6, Rev: 5)
				BRD2-DMA-2_R1	TCCGCGAGTTACCTTGCCTCACTTGT				
<i>DMA</i>	162776 - 164862	2087		DMA_F1	CCTCTGGACGCGTTTGTCTATTGC	68	3160	<i>DMA_e1~e4</i>	10 (Fwd: 5, Rev: 5)
				DMA_R2	CTTCATCCCTCCGTGCCACC				
<i>DMB1</i>	165247 - 167026	1780		DMB1_F4	GGGCTTCATGCGCTTCTCCTACCTG	68	3527	<i>DMB1_e1~e6</i>	13 (Fwd: 6, Rev: 7)
				DMB1_R5	AAAGGCTGAGCCCAACCTAAAGCCCT				
<i>DMB2</i>	167630 - 170566	2937		DMB2_F1	GAAACAGATGACGCTACCACGG	68	3153	<i>DMB2_e1~e5</i>	26 (Fwd: 12, Rev: 14)
				DMB2_R1	TCTTTAATGTCAGCACCACGGCG				
				DMB2_F1	GAAACAGATGACGCTACCACGG	68			
				DMB2_R1B21	TCTTTAATGTCAGCACCACGGTG				
<i>BF1</i>	171383 - 173416	2034		BF1_F1	CCTATTCGCCCAACAGGTTACGCCCC	68	4015	<i>BF1_e1~e8</i>	21 (Fwd: 10, Rev: 11)
				BF1_R3	ACAAGGACCCACAAGAGCTGTGCC				
<i>TAP1</i>	174535 - 179331	4797		TAP1_F2	GGGTAAGGATGGGTATAGGCTGGGCACT	68	4727	<i>TAP1_e1~e11</i>	27 (Fwd: 15, Rev: 12)
				TAP1_R1	CAGTGGCACCAGTCCATGC				
			<i>TAP1-TAP2</i>	TAP1-TAP2-F1	TCCCACCCTGTCTTCAATCC	60	899		
				TAP1-TAP2-R1	CAGTGCCTTTTGAACGGCCC				
<i>TAP2</i>	179887 - 182923	3037		TAP2-F2	CCTGATCACACAGAACAACACTGCAAC	68	4568	<i>TAP2_e1~e9</i>	31 (Fwd: 16, Rev: 15)
				TAP2-R2	TGATTGAAAGTAAAAGTAACGGCG				
				TAP2-F1B21	TCCAAACCCACATCATTCCCATT	68			
				TAP2-R1B21	CTACAAGGATCCAACCTTGTGGACAG				
<i>BF2</i>	185287 - 187303	2017		BF2_F2	TTCCATCGGGTGTCTTCCGCC	68	5339	<i>BF2_e1~e8</i>	21 (Fwd: 11, Rev: 10)
				BF2_R5	CCTGATCCCAAGGAAGCCCTGG				

The locations within the amplified regions were calculated using the 241 kb red jungle fowl B21 genomic sequence (accession number; AB268588). The length on the right side indicates non-redundant amplified segments, and "e" in "included exon" column indicate exons. Locations of amplicons were indicated to Fig. 1.

Sup Table 1B. Sequencing primers

Gene region	Intergenic region	Primer number	Sense primer	Primer number	Antisense primer
<i>BG1</i>		1	TACAAACACTGTCTCCTCT	12	GATTATCCTCAGTACCCAA
		2	TATATACCATCGCCCTG	13	AATTCACAGTGGAGTAAGC
		3	ATGACTGCAGCTTACTCC	14	TTCAGATCTGGGTGAGTCCT
		4	TGCATGATGAGAAGGGTCAG	15	CCTTTGCAGAGAGAAGGGAT
		5	TCACCCAGATTTTCAACT	16	ACTAGCTTCAGAACTGGGTG
		6	CTCATCCACTATCGCAG	17	AACTACCTGCGATAGTGG
		7	CACTCTGCAGTCTTCTATC	18	GAGACCACAAAGCAGAGT
		8	AAAGCAAGACTCAGCCT	19	GTCACAATTCTGGTTGG
		9	CTCCCTTTATATTCCTCC	20	TTTGTGGATAAGTCTGCA
		10	ACGAGATAAGGCAGGAG	21	CACTTTGGTTATTCATG
		11	GATGAGAGACGAAGATAGG	22	CTCCTATTTCCCTGATCT
<i>Blec4</i>		1	TTTCCCTACAAAGAGC	11	CTTATCTCGTGGCTCTG
		2	GTTGGAGAACATAAAACAC	12	CCCATTTTTTTTTACCC
		3	TCTCAATTTCTCCTGTATC	13	TCAGGTGAAGGATTTCT
		4	CCCTAAGAATCAGTGCA	14	CCTCACTGTGAATGCAC
		5	CGCAGTTCTGTTGGTTA	15	TTTCGACACCTTTCCT
		6	ACCAAATATTGCCTTTC	16	AATTTATTTGCAGTCCC
		7	ACTTCTGAGCCATGGAT	17	CTACAGCCTTTCCTTC
		8	GAACTGGAGGAAAACAA	18	TTCCATTCTCTCACATTG
		9	GATGAACCATTTTTGTAGG	19	ACAAATGACCCGATTCTGT
		10	GTGAGCTGATTGCATGA	20	CATTTCTTTTCTCTTCCTG
<i>Blec2</i>		1	GCAAACAGATGCATTCT	11	ATCCATAATGTGCAGGA
		2	CTCACTCTGTGCTGTTGTA	12	AAATCTGCAGTCTCAGC
		3	CCTAAAGGGCATAATCC	13	TGATCACACAACAATTCC
		4	AGTCTGCCTTGTGGAC	14	ATGTCCTGTGTCCATC
		5	TGGTTGCACTCAATTAA	15	TCTGAGAAAACCCAGCA
		6	GGATCTGATCACTCACC	16	CAGAGAGCAGCAAAATG
		7	GATGGACACAGGGACAT	17	GTTGGTTAACGCTTTTTCT
		8	CTCAGAAAGTTCACGAGAA	18	GCAATTCTGGTAAATGAG
		9	GGAAGAAAGGCAATATT	19	CTAAGAATCAGTGCATCCT
<i>Blec1</i>		1	TCCTTTGCATATTGCTG	12	ATAACCTCTCCCTCCCT
		2	TGCAGCATCCACGTGGAAT	13	GAGGACTGAAATTAATGC
		3	CAGGTGGTAACAATGAAA	14	GATGTGTTAAGGGCATG
		4	GCACCCAGAAATATATCC	15	GTGAGCTGGAAGGTAAC
		5	TGCGATTCTGTGATGTT	16	GTCCACAGACCTCTTG
		6	GAGCAGAGAAAACCCCT	17	TAGTAGCATTTTCCCTCTGA
		7	AATGATGAGTAATCCACC	18	AATCTCAGTGCCTTGAACCT
		8	GATGAGAGCAATTGGAC	19	ATGAACCTCTATGACCCA
		9	GCTTCACAATGAGACACA	20	TCCTGTGCTACTGAGC
		10	TTGATTTCACTACTGTG	21	CAGTATTTCCCTTTGGAG
		11	CTAATGACCGCTAAAATC		
<i>BLB1</i>		1	CTAATGACCGCTAAAATC	14	CACCGTAAAAGTGAATTC
		2	GGAATAGAAGAGCACAGAC	15	ATGCTGAATTAGCTGCT
		3	ATGCGAACGGGAACGGGAAT	16	GGAGATCGAGGTGAAGT
		4	ACCTGGTACGTCCAGTC	17	AGTGCCACTACCTGAAC
		5	TCATTCAITCGGTTCTC	18	GAGTGTGAGGAAAGCC
		6	GTTGAGGTAGTGGCACT	19	GATGAGCACTGGATGAC
		7	TTCTCTGACTACTCTGC	20	AGAAACCCCGGAGCCCTTC
		8	GGCTATCCGTGCGCTG	21	CCGTGCTGGTGGCACT
		9	CTTCTGGTGATTTTATGCAA	22	GCACTGGATGACCATGGAG
		10	GCAGCTAATTCAGCATCCCT		
		11	CCGAGACCCCTCACCTTGG		
		12	TGCGCACGGCCAGAAG		
		13	GCTCCCCATGGCTGCT		
<i>BLB1-TAPBP</i>		1	GTAACCCCATGTTCCACC	6	AACGAAAAGGTAACCAC
		2	TGTCACCCAGATGTCCACAA	7	CAAAGTTCTCTCTGTGT
		3	CAATGTCATCCAGGTGTCCA	8	AAGGTGAGTGTGTTCC
		4	GGAATGAGAATGGTGAG		
		5	GGAACAGCACTCACCTT		
<i>TAPBP</i>		1	GGCGTCTTCCACCCTAAATT	19	ACAGAAGGAACCATCACTGC
		2	AACTGTCATAGGCCAGCAGG	20	ACTGCACTGGCCAAACCAAT
		3	TAGAAGCCAGACACGTGGCA	21	CCTTTACTTCCCACAATGCT
		4	TTTAGGGTAGAGCCAACGGA	22	GTGTTTCCATGTCCCCTCAT
		5	GGGACAGTTTGGGAGCTATT	23	GGTCAGATAGGACATATGGG
		6	CATGAGGACAGGGAGAAACT	24	TCCAAGCACCCCAAACTCA
		7	GACAAAAGATGCAGAGGAGCA	25	CAAACACTGTTCTGAATGA
		8	GAGAGAACTTTGGGGTGAAA	26	ACTGTGCCCTTTGGGGGGG
		9	AGCCGCAGCCCCGAGCCAT	27	AACCCCGAGCCGGCTCTGA
		10	CAGTGATGGTTCTTCTGTG	28	AGACAGTGTGCAGCTCCAC

	11	AAGGCGCAGTGCAGGTGGAT	29	ATGGAACCTACAGCCGGACG
	12	TTCTTCGGGGACAGCGTCAC	30	CCTTGCAGAAATCGCAGTGA
	13	ATGAGGCCACAGAGGACAAA	31	CACCAATGTCCCCAAATCC
	14	ATGGGAGCATTGTGGGAAGT	32	TTCACCTCCCCATGTCCCC
	15	GACGTAAGGATGAGGTTCCA	33	TATTGACGAAGTGACGGAGGGG
	16	TCACCAACCCAGGACTTCCT	34	AAAGCAGCGGAGAGCGATGG
	17	CGCTGACATTGAAGGTGACT	35	TCACAGTGGCCCTGGCGGTG
	18	CAAAGACGTGGAGCTGCAGC		
<i>BLB2</i>	1	TTTAAATCCTGAAACC	10	CCTCATCCTTAGCTCAC
	2	GCAGAAAATGGTGTGAC	11	GATGGTCTCCAATGAC
	3	TGAGCACTGGATGACCATG	12	GCGTTGCTGTTCCAGTATTC
	4	ATCTACAACCGCAGCAGTT	13	CTGAAACACAGCGAGAC
	5	GACTGGACGTACCAGGT	14	GCAGCTAATTCAGATCCCT
	6	GTCTCGCTGTGTTTCAG	15	CCGAGACCCTCACCTTGG
	7	AGAAACCCCGGAGCCCTTC	16	TGCGCACGGCCAGAAG
	8	CCGTGCTGGTGGCACT	17	GCTCCCCATGGCTGCT
	9	GCACTGGATGACCATGGAG		
<i>BLB2-BRD2</i>	1	GGATGCTGAATTAGCTG	5	CAGCGGTTTTATTAGGATGG
	2	TATGGATAACCCAAAGC	6	GTGACAAATGACACAGCA
	3	GAAAAAATCCACGAGT		
	4	AACAAACAGTAAAACCTGC		
<i>BRD2</i>	1	AACAAACAGTAAAACCTGC	9	TTAAACCCACAGCACCACA
	2	TCATGGCTGTGAAATTC	10	GTGCACATCATCCAGTC
	3	TTTTGGTTTTGAAACGGGG	11	GATGAGGATGAGAGCAGTAG
	4	AACATTAACCGGACATCAGCG	12	AAACCCCAAGAAGGACTT
	5	GAATCCGGCAAGTCTTCTT	13	CAGATGACATTGTGCTG
	6	AAGGTTGATGAATGGAGGC	14	CTTTAGCAATTAGTGCC
	7	GGTTTTAGGAGCTCAA	15	AAGTGGTGAAGGCCCTG
	8	GGATTATGCCCTAAGA		
<i>BRD2-DMA-1</i>	1	TATGCCCTAAGAGAGG	7	TAATCCAACTCCACAG
	2	AGGGAGCAAAAGACAAC	8	CCCAGCTGCTAAATCCTCA
	3	AGAATTCACATGGACCA	9	GGTCCATGTGAATTCTGT
	4	TCTGTGCTATGCACCTC	10	CATCAGTTGTATCCCACT
	5	TCATAACTGCCAACACC	11	CGTTTGTCTCGTTTATGTG
	6	TTATATAGACACCACCTGG	12	TCTATCCGGTTCTTACC
<i>BRD2-DMA-2</i>	1	TTCACATTCTGCAGCAT	7	TTTCCCGCTCTATATC
	2	GTCCGCAATTTGTGTGGC	8	CTCACTACCTCACCACAG
	3	TCTTTTAGTTTCTCAAGGC	9	GAAATTCCTGTGAGGTG
	4	AAAGGCTCTCAAAGACC	10	TCCATCAAATCTGGTTC
	5	ACATCCAGGGCAGAAAAAG	11	AATGACAAACGCGTCCAGAG
	6	CACAAGACACATTTTTACC		
<i>DMA</i>	1	CCCCAAAAACATACTTT	6	CTGCTGTCTCCATTGTC
	2	GCACTCTGGTACATCTAT	7	CGCAAGCAATTAATAAG
	3	ATTGGCTAAACTGGTTG	8	ATCTCACTCAACCCC
	4	AGCTCTTCTCATTGATG	9	ATTCTGTGAGCAAATC
	5	TGTGTTCCCAATGGACATCC	10	CATCAGTGAGGACACATCGT
<i>DMB1</i>	1	GGTTCTCACTCCAATCC	7	GGAACGAAGAATTGGAG
	2	GGAACAGATGACGCTA	8	CCTACCATGATCCCATA
	3	CCCGTACTCACTGATGT	9	ATCAGACTTTGCCACCT
	4	TTTTAGGGTGCAACATGGGG	10	GTGGTATCATCATTAGGA
	5	GCATGAGGAAGTGAAG	11	CACTCAATTTGTTGCA
	6	CACCTACACATGCTCAG	12	CTGACAGAAAGCTGAAAAC
<i>DMB2</i>	1	TCTCTGCCTAATGAAACTC	13	GAGTTTCATTAGGCAGAGA
	2	CAATATTGAGGACACTCTG	14	ACAGTCTTCCCAGAACC
	3	GATTTTGGAGTGATGCT	15	CAGAGTGTCTCAATATTG
	4	AGCTCGATGTTATGTCC	16	AGCATCACTCCAAAATC
	5	ACCCTCTGGTGTGCTAC	17	TCCCATGAGATTCTTAAAG
	6	GTGGCTTTGAAGAACAT	18	TGCTGTCATTGTTGAGG
	7	ATGGAGTTTGCTTCAAG	19	TGCTAAACAACACCCTC
	8	GGAAGTGGACCTACCAG	20	ATGTTCTTCAAAGCCAC
	9	CAGCTTGCTCTTCATTG	21	CTTGAAGCAAATCCAT
	10	GGTATCTGTTGATCCCTAT	22	CATCTCACTTCCCTGTAG
	11	GGTCACAACCTACCCTTC	23	CTGGTAGGTCCAGTTCC
	12	CGCAGGAGTGAGCAT	24	CAATGAAGAGCAAGCTG
			25	CAAAAATGGTCAATCC
			26	GACTGTTACCTGAAGG
<i>BF1</i>	1	TTAAGGAGGGGACAACAGTG	11	AGGCAGAATGCGCTCCCTCAG
	2	CTGGCGCCGATGACGTCA	12	TGAGCCGCGGGTGGGGGTCT
	3	AGATCGGACAGGGCAATGAG	13	TAGTGCACGAAGATTTCCCG
	4	TGGGAGCCCGGAGC	14	GCTCCGGGGTCCCA
	5	AGATACGTGAATACGGGAAGG	15	CCTTCCCGTATTCCAGTATCT
	6	CCGTGCCATTGTGGC	16	GCCACAATGGCGACGG
	7	GGATCCAGCAGCTCGAGC	17	CAAAGCACCAGGAATGGG

8	TGCTGACTGTTATGCTTTGCCTG	18	CATAGGAAGCAGAATGAGATGTGAG
9	TTCTGCACTGTGCTGTGGTT	19	TGGGAAAATGAGAGTTCTGCCA
10	TGGCAGAACTCTCATTTTCCCA	20	GAGGGCAGCAGAACAACAT

21	AAAGCCGCATGTTTGTACCC
16	ATAGCGGGAGTTATGGATGGG
17	TCATACTCGACGAGCACACCAG
18	GATATGAAACAAGGAGATACATGGAGG
19	GAACCCGCTCTCAAGGTGG
20	TGCTGCACTACTTCCCACAC
21	GGACCTCGTCACCTTCTCTCC
22	GACATTGACAGAACAGGAAGGTGAC
23	GGACCAGTGGTGTATGGGATG
24	TGTGCGAAGCTTTGCCAA
25	CATTATCCCTTCCACATGGGTT
26	GCTCACCGCGCTGGC

TAP1

1	GTGGGAGGAGAAACGGTCAG
2	GGCAGGCGAGTGATGAAGTC
3	AACCCATAGGAGATGTTGGCG
4	AGGTAGGAGTGCTGGTAGGCG
5	AGCTCCAGTGATACGCCCTG
6	CCACCTTGAGGACGGGTTTC
7	CGGTCCAGGAACTCAAAGATCT
8	GGAGGAAGGTGACGAGGTCC
9	ACCTTCTGTTCTGTCAATGTCC
10	GTGCATGTATGGAGGGAACA
11	GCACATGGATAGGGCAATGA
12	GCACGTCTCCGCATCC
13	GACGCGGCGCTGGAG
14	CAGTACCTGCTGAGGCCCAG
15	CACCCCAAAGCTCAGAGG

TAP1-TAP2

1	TCCCACCTGTCTTCAATCC
1	GTTGTGTGCTCCAGGCTGG
2	CGATGCCGCCCTACATTCTGCG
3	GCCCCGCATCTTCTGACC
4	GGCAAAGGAGGCAGAGGCC
5	TCTGGATGTCTCCGCCA
6	TGACCCTTTGTGATTGT
7	GTTGGCACTCAATACAA
8	ACGGAAGTCTATGACAC
9	CACAGCAAGGATGAGAG
10	AGTGCAGGAGTCCATCT
11	CACTGGCGTACTCCTAT
12	TGGAGAGATTCTATGAACC
13	GGATAACATTGCCTACG
14	AATGGTGAGCACTGAGCAGT
15	CACTGAGAACCATGGAG
16	TCTCCATATGAAAGCCA

TAP2

2	CAGTGCTTTTAGAACGCCCC
17	CTTCCAGTCCGGCTCCCCACAG
18	GGTCAGGAAGATGGC
19	GGCCTCTGCCTCCTTTGC
20	GCGGAGGACATCCAG
21	CCCAGATATGGACAGAG
22	TTGATATTGAGTGCCAA
23	CTCTCATCCTTGTCTGTG
24	AGATGGACTCCTGCACT
25	ATAGGAGTACGCCAGTG
26	TCCCAGTTCAGGTAATC
27	GGTTCATAGAATCTCTCCA
28	CAATGTTATCCCGAATG
29	CTCCATGGTTCAGTG
30	TCTGGAGATACTCAAAGCCC
31	TGGCTTTCATATGGAGA

BF2

1	AAAGCCGCATGTTTGTACCC
2	TGGGAAAATGAGAGTTCTGCCA
3	CCAAGCACCCAGGAATGGG
4	GCCACAATGGCGACGG
5	CGGCAGTGAGGGCCG
6	CCTTCCGTATTCCACGTATCT
7	GCTCCGGGGCTCCCA
8	TAGTGCACGAAGAGTTCCCCG
9	GCTGCACTCTCAAGTCCGC
10	AGGCAGAAATGCCTCCCTCAG

11	CAGTCCCGCAGAAGGCTG
12	TGGCAGAACTCTCATTTTCCCA
13	TTCTGCACTGTGCTGTGGTT
14	TGCTGACTGTTATGCTTTGCCTG
15	GGATCCAGCAGCTCGAGC
16	CCGTGCGCCATTGTGGC
17	AGATACGTGGAATACGGGAAGG
18	TGGGAGCCCCGGAGC
19	AGATCGGACAGGGCAATGAG
20	GAGTAGGAAAAGCTGAAGGAGCTG
21	CTGGCGCCCCGATGACGTCA